

Leafy Green Project: Reducing the Risk for Transfer of Zoonotic Foodborne Pathogens from Domestic and Wild Animal to Vegetable Crops in the Southwest Desert

In May 2010, an outbreak of *Escherichia coli* O145 infections was linked to Romaine lettuce grown in the desert southwest. This was the first known leafy green-related shiga toxin-producing *Escherichia coli* (STEC) outbreak traced to the region. Based on initial investigations by the Center for Disease Control (CDC) and the Food and Drug Administration (FDA) following the outbreak, pre-harvest contamination was suspected, although no laboratory confirmed source was determined.



The role of domestic and wildlife animals as reservoirs and transmitters of bacterial pathogens to fresh produce has been studied at length in some growing regions, such as the California central coast. In contrast, limited information exists on the importance of animal sources of contamination in the desert southwest growing region (DSGR). This project will help identify domestic and wildlife animal reservoirs of STEC and *Salmonella* in the DSGR, a major fresh vegetable production region of the US-Mexico border that is second only to central California in terms of lettuce production.

Results from this research will provide baseline prevalence, diversity, and distribution data for STEC and *Salmonella* in terrestrial and avian species in the DSGR. It may also indicate important risk factors for the transfer of pathogenic bacteria strains from animal operations to produce fields by wildlife. Thus, our findings may influence wildlife risk assessments as well as environmental management decisions for reducing the risk of pre-season and pre-harvest contamination caused by wildlife intrusions while also minimizing environmental impacts on wildlife.

Objectives

1. To determine if domestic animals and terrestrial and avian wildlife species in the desert southwest produce production region are reservoirs of STEC or *Salmonella*. We will utilize livestock surveys, and hunter-harvested and targeted sampling and testing of feces and colon from terrestrial and avian wildlife species to assess the potential pathogen burden of these animals.
2. To determine the extent to which wildlife and cattle share genetically related strains of STEC and *Salmonella*, and measure the movement of strains from livestock operations to produce fields by wildlife populations. We will utilize intensive trapping and radio telemetry with spatial analysis to assess animal movements and the potential spread of pathogens. Molecular genotyping will provide a comparison of the genetic relatedness of strains isolated from these animals with strains from nearby livestock.
3. Extend knowledge of preventing produce contamination by domestic animals and terrestrial and avian wildlife populations to the produce and livestock communities. We will share the knowledge gained from this study with the produce industry, conservation groups, and other stakeholders to improve best practices for pre-season and pre-harvest environmental assessments and wildlife intrusion, and no-harvest buffer zones.

These objectives will be met by utilizing partnerships with the Western Center for Food Safety, University of California, Davis and local industry collaborators. Hypotheses will be tested through bacteriologic and molecular microbiologic approaches, and spatial and statistical epidemiologic analysis.

Project contacts

Anne Justice-Allen, DVM, Wildlife Health Specialist, 623-236-7351, ajustice-allen@azgfd.gov
Carrington Knox, Wildlife Disease Biologist, 623-236-7674, cknox@azgfd.gov